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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/602,874C

DATE: 03/13/2002

TIME: 11:29:18

Input Set : A:\seqlistcorr3.txt

Output Set: N:\CRF3\03132002\I602874C.raw

3 <110> APPLICANT: Pompejus, Markus  
4 Kroger, Burkhard  
5 Schroder, Hartwig  
6 Zelder, Oskar  
7 Haberhauer, Gregor  
9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
10 REGULATORY PROTEINS  
12 <130> FILE REFERENCE: BGI-123CP  
14 <140> CURRENT APPLICATION NUMBER: US 09/602,874C  
15 <141> CURRENT FILING DATE: 2000-06-23  
17 <150> PRIOR APPLICATION NUMBER: 60/141031  
18 <151> PRIOR FILING DATE: 1999-06-25  
20 <150> PRIOR APPLICATION NUMBER: 60/142690  
21 <151> PRIOR FILING DATE: 1999-07-01  
23 <150> PRIOR APPLICATION NUMBER: 60/151251  
24 <151> PRIOR FILING DATE: 1999-08-27  
26 <150> PRIOR APPLICATION NUMBER: DE 19930476.9  
27 <151> PRIOR FILING DATE: 1999-07-01  
29 <150> PRIOR APPLICATION NUMBER: DE 19931419.5  
30 <151> PRIOR FILING DATE: 1999-07-07  
32 <150> PRIOR APPLICATION NUMBER: DE 19931420.9  
33 <151> PRIOR FILING DATE: 1999-07-08  
35 <150> PRIOR APPLICATION NUMBER: DE 19932122.1  
36 <151> PRIOR FILING DATE: 1999-07-09  
38 <150> PRIOR APPLICATION NUMBER: DE 19932128  
39 <151> PRIOR FILING DATE: 1999-07-09  
41 <150> PRIOR APPLICATION NUMBER: DE 19932206.6  
42 <151> PRIOR FILING DATE: 1999-07-09  
44 <150> PRIOR APPLICATION NUMBER: DE 19932207.4  
45 <151> PRIOR FILING DATE: 1999-07-09  
47 <150> PRIOR APPLICATION NUMBER: DE 19933003.4  
48 <151> PRIOR FILING DATE: 1999-07-14  
50 <150> PRIOR APPLICATION NUMBER: DE 19941390.8  
51 <151> PRIOR FILING DATE: 1999-08-31  
53 <150> PRIOR APPLICATION NUMBER: DE 19942088.2  
54 <151> PRIOR FILING DATE: 1999-09-03  
56 <150> PRIOR APPLICATION NUMBER: DE 19942124.2  
57 <151> PRIOR FILING DATE: 1999-09-03  
59 <160> NUMBER OF SEQ ID NOS: 362  
61 <210> SEQ ID NO: 1  
63 <211> LENGTH: 514  
64 <212> TYPE: DNA  
65 <213> ORGANISM: Corynebacterium glutamicum

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67 <220> FEATURE:
68 <221> NAME/KEY: CDS
69 <222> LOCATION: (101)..(514)
70 <223> OTHER INFORMATION: RXN03181
72 <400> SEQUENCE: 1
73 gtcgcaaaag tcgctggcgt ctcccccttcc actgtgtgcg gggcggttttc gcagcctggg 60
75 cgagtgcggtt tttccactgc ggagaaaatc cgcaacgcgt gtg gaa act cag gct 115
76                                     Val Glu Thr Gln Ala
77                                     1           5
79 ttt cag cgc caa aac acc ggc ctc atc gct atg gtt gcc gcc gat gcg 163
80 Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met Val Ala Ala Asp Ala
81             10             15             20
83 tcg aat ccc ttc ttc ttg gaa att ttc cgg ggc gcg cag cac gcc gca 211
84 Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala
85             25             30             35
87 agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259
88 Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala
89             40             45             50
91 att aag tcc agg gag gtg ctg gac aag atc gtc ccc cac gcc gat ggc 307
92 Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly
93             55             60             65
95 tta ttg ctc gct gct tca agg atg gat tct ggt gag atc cac aaa gtc 355
96 Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val
97 70             75             80             85
99 gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att 403
100 Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile
101             90             95             100
103 ccc agc gtg atg gtg gat aac tac gac ggt gcg ccg aag gct gtg gtg 451
104 Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val
105             105             110             115
107 cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct 499
108 His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr Tyr Ile Ala Gly Pro
109             120             125             130
111 aat aaa tcc tgg gct 514
112 Asn Lys Ser Trp Ala
113             135
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 138
118 <212> TYPE: PRT
119 <213> ORGANISM: Corynebacterium glutamicum
121 <400> SEQUENCE: 2
122 Val Glu Thr Gln Ala Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met
123 1           5           10           15
125 Val Ala Ala Asp Ala Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly
126             20             25             30
128 Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp
129             35             40             45
131 Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val
132             50             55             60

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134 Pro His Ala Asp Gly Leu Leu Ala Ala Ser Arg Met Asp Ser Gly
135 65 70 75 80
137 Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg
138 85 90 95
140 Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala
141 100 105 110
143 Pro Lys Ala Val Val His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr
144 115 120 125
146 Tyr Ile Ala Gly Pro Asn Lys Ser Trp Ala
147 130 135
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 514
152 <212> TYPE: DNA
153 <213> ORGANISM: Corynebacterium glutamicum
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (101)..(514)
158 <223> OTHER INFORMATION: FRXA02880
160 <400> SEQUENCE: 3
161 gtcgcaaaag tcgctggcgt ccccccttcc actgtgtcgc gggcggttttc gcagcctggg 60
163 cgagtgaagt tttccactgc ggagaaaatc cgcaacgcgt gtg gaa act cag gct 115
164 Val Glu Thr Gln Ala
165 1 5
167 ttt cag cgc caa aac acc ggc ctc atc gct atg gtt gcc gcc gat gcg 163
168 Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met Val Ala Ala Asp Ala
169 10 15 20
171 tcg aat ccc ttc ttc ttg gaa att ttc cgg ggc gcg cag cac gcc gca 211
172 Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala
173 25 30 35
175 agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259
176 Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala
177 40 45 50
179 att aag tcc agg gag gtg ctg gac aag atc gtc ccc cac gcc gat ggc 307
180 Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly
181 55 60 65
183 tta ttg ctc gct gct tca agg atg gat tct ggt gag atc cac aaa gtc 355
184 Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val
185 70 75 80 85
187 gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att 403
188 Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile
189 90 95 100
191 ccc agc gtg atg gtg gat aac tac gac ggt gcg ccg aag gct gtg gtg 451
192 Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val
193 105 110 115
195 cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct 499
196 His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr Tyr Ile Ala Gly Pro
197 120 125 130
199 aat aaa tcc tgg gct 514
200 Asn Lys Ser Trp Ala

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201      135
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 138
206 <212> TYPE: PRT
207 <213> ORGANISM: Corynebacterium glutamicum
209 <400> SEQUENCE: 4
210 Val Glu Thr Gln Ala Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met
211      1          5          10          15
213 Val Ala Ala Asp Ala Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly
214          20          25          30
216 Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp
217          35          40          45
219 Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val
220          50          55          60
222 Pro His Ala Asp Gly Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly
223      65          70          75          80
225 Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg
226          85          90          95
228 Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala
229          100         105         110
231 Pro Lys Ala Val Val His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr
232          115         120         125
234 Tyr Ile Ala Gly Pro Asn Lys Ser Trp Ala
235          130         135
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 576
240 <212> TYPE: DNA
241 <213> ORGANISM: Corynebacterium glutamicum
243 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (101)..(553)
246 <223> OTHER INFORMATION: RXA00603
248 <400> SEQUENCE: 5
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251 ttgccagttt gcgcacctca actaggctat tgtgcaatat atg aag cta gat tcc 115
252                               Met Lys Leu Asp Ser
253                               1          5
255 att gat cgc gca att att gcg gag ctt agc gcg aat gcg cgc atc tca 163
256 Ile Asp Arg Ala Ile Ile Ala Glu Leu Ser Ala Asn Ala Arg Ile Ser
257          10          15          20
259 aat ctc gca ctg gct gac aag gtg cat ctc act ccg gga cct tgc ttg 211
260 Asn Leu Ala Leu Ala Asp Lys Val His Leu Thr Pro Gly Pro Cys Leu
261          25          30          35
263 agg agg gtg cag cgt ttg gaa gcc gaa gga atc att ttg ggc tac agc 259
264 Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile Ile Leu Gly Tyr Ser
265          40          45          50
267 gcg gac att cac cct gcg gtg atg aat cgt gga ttt gag gtg acc gtg 307
268 Ala Asp Ile His Pro Ala Val Met Asn Arg Gly Phe Glu Val Thr Val
269          55          60          65

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271 gat gtc act ctc agc aac ttc gac cgc tcc act gta gac aat ttt gaa 355
272 Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr Val Asp Asn Phe Glu
273 70 75 80 85
275 agc tcc gtt gcg cag cat gat gaa gta ctg gag ttg cac agg ctt ttt 403
276 Ser Ser Val Ala Gln His Asp Glu Val Leu Glu Leu His Arg Leu Phe
277 90 95 100
279 ggt tcg cca gat tat ttt gtc cgc atc ggc gtt gct gat ttg gag gcg 451
280 Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val Ala Asp Leu Glu Ala
281 105 110 115
283 tat gag caa ttt tta tcc agt cac att caa acc gtg cca gga att gca 499
284 Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr Val Pro Gly Ile Ala
285 120 125 130
287 aag atc tca tca cgt ttt gct atg aaa gtg gtg aaa cca gct cgc ccc 547
288 Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val Lys Pro Ala Arg Pro
289 135 140 145
291 cag gtg tgaagcatgc attttgaagc atg 576
292 Gln Val
293 150
296 <210> SEQ ID NO: 6
297 <211> LENGTH: 151
298 <212> TYPE: PRT
299 <213> ORGANISM: Corynebacterium glutamicum
301 <400> SEQUENCE: 6
302 Met Lys Leu Asp Ser Ile Asp Arg Ala Ile Ile Ala Glu Leu Ser Ala
303 1 5 10 15
305 Asn Ala Arg Ile Ser Asn Leu Ala Leu Ala Asp Lys Val His Leu Thr
306 20 25 30
308 Pro Gly Pro Cys Leu Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile
309 35 40 45
311 Ile Leu Gly Tyr Ser Ala Asp Ile His Pro Ala Val Met Asn Arg Gly
312 50 55 60
314 Phe Glu Val Thr Val Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr
315 65 70 75 80
317 Val Asp Asn Phe Glu Ser Ser Val Ala Gln His Asp Glu Val Leu Glu
318 85 90 95
320 Leu His Arg Leu Phe Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val
321 100 105 110
323 Ala Asp Leu Glu Ala Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr
324 115 120 125
326 Val Pro Gly Ile Ala Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val
327 130 135 140
329 Lys Pro Ala Arg Pro Gln Val
330 145 150
333 <210> SEQ ID NO: 7
334 <211> LENGTH: 582
335 <212> TYPE: DNA
336 <213> ORGANISM: Corynebacterium glutamicum
338 <220> FEATURE:
339 <221> NAME/KEY: CDS

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VERIFICATION SUMMARY

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